ABSTRACT OF THE DISCLOSURE

Methods to design vaccines which are effective in individuals bearing A2 supertype alleles are described. Single amino acid substitution analogs of known A2-supertype binding peptides, and large peptide libraries were utilized to rigorously define the peptide binding specificities of A2-supertype molecules. While each molecule was noted to have unique preferences, large overlaps in specificity were found. The presence of the hydrophobic and aliphatic residues L, I, V, M, A, T, and Q in position 2 of peptide ligands was commonly tolerated by A2-supertype molecules. L, I, V, M, A, and T were tolerated at the C- terminus. While examination of secondary influences on peptide binding revealed allele specific preferences, shared features could also be identified, and were utilized to define an A2-supermotif. Shared features also correlate with cross-reactivity; over 70% of the peptides that bound A*0201 with high affinity were found to bind at least 2 other A2-supertype molecules. Finally, the coefficients for use in the development of algorithms for the prediction of peptide binding to A2-supertype molecules are provided.